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SEQUENCE LISTING

<110> Johansen, Teit E.

Blom, Nikolaj

Hansen, Claus

<120> Novel Neurotrophic Factors

<130> 19313-001 DIV

<140> U.S.S.N 09/662,183

<141> 2000-09-14

<150> DANISH 1998 00904

<151> 1998-07-06

<150> USSN 60/092,229

<151> 1998-07-09

<150> DANISH 1998 01048

<151> 1998-08-19

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<150> DANISH 1998 01260

<151> 1998-10-05

<150> USSN 60/103,908

<151> 1998-10-13

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<151> 1998-10-06

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<151> 2000-07-02

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tccccaagcc cacctgggtg ccctctttct ccctgaggct ccacttggtc tctccgcgc 119

atg	cct	gcc	ctg	tgg	ccc	acc	ctg	gcc	gct	ctg	gct	ctg	ctg	agc	agc	167
Met	Pro	Ala	Leu	Trp	Pro	Thr	Leu	Ala	Ala	Leu	Ala	Leu	Leu	Ser	Ser	
-95					-90					-85				-80		
gtc	gca	gag	gcc	tcc	ctg	ggc	tcc	gcg	ccc	cgc	agc	cct	gcc	ccc	cgc	215
Val	Ala	Glu	Ala	Ser	Leu	Gly	Ser	Ala	Pro	Arg	Ser	Pro	Ala	Pro	Arg	
				-75					-70					-65		
gaa	ggc	ccc	ccg	cct	gtc	ctg	gcg	tcc	ccc	gcc	ggc	cac	ctg	ccg	ggg	263
Glu	Gly	Pro	Pro	Pro	Val	Leu	Ala	Ser	Pro	Ala	Gly	His	Leu	Pro	Gly	
			-60					-55					-50			
gga	cgc	acg	gcc	cgc	tgg	tgc	agt	gga	aga	gcc	cgg	cgg	ccg	cgc	cgc	311
Gly	Arg	Thr	Ala	Arg	Trp	Cys	Ser	Gly	Arg	Ala	Arg	Arg	Pro	Arg	Arg	
		-45					-40						-35			
aga	cac	ttc	tcg	gcc	cgc	gcc	ccc	gcc	gcc	tgc	acc	ccc	atc	tgc	tct	359
Arg	His	Phe	Ser	Ala	Arg	Ala	Pro	Ala	Ala	Cys	Thr	Pro	Ile	Cys	Ser	
	-30					-25					-20					
tcc	ccg	cgg	gtc	cgc	gcg	gcg	cgg	ctg	ggg	ggc	cgg	gca	gcg	cgc	tcg	407
Ser	Pro	Arg	Val	Arg	Ala	Ala	Arg	Leu	Gly	Gly	Arg	Ala	Ala	Arg	Ser	
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ggc	agc	ggg	ggc	gcg	ggg	tgc	cgc	ctg	cgc	tcg	cag	ctg	gtg	ccg	gtg	455
Gly	Ser	Gly	Gly	Ala	Gly	Cys	Arg	Leu	Arg	Ser	Gln	Leu	Val	Pro	Val	
			5					10					15			
cgc	gcg	ctc	ggc	ctg	ggc	cac	cgc	tcc	gac	gag	ctg	gtg	cgt	ttc	cgc	503
Arg	Ala	Leu	Gly	Leu	Gly	His	Arg	Ser	Asp	Glu	Leu	Val	Arg	Phe	Arg	
		20					25					30				
ttc	tgc	acc	ggc	tcc	tgc	ccg	cgc	gcg	cgc	tct	cca	cac	gac	ctc	agc	551
Phe	Cys	Thr	Gly	Ser	Cys	Pro	Arg	Ala	Arg	Ser	Pro	His	Asp	Leu	Ser	
	35						40				45					
ctg	gcc	agc	cta	ctg	ggc	gcc	ggg	gcc	ctg	cga	ccg	ccc	ccg	ggc	tcc	599
Leu	Ala	Ser	Leu	Leu	Gly	Ala	Gly	Ala	Leu	Arg	Pro	Pro	Pro	Gly	Ser	
50					55					60					65	
cgg	ccc	gtc	agc	cag	ccc	tgc	tgc	cga	ccc	acg	cgc	tac	gaa	gcg	gtc	647
Arg	Pro	Val	Ser	Gln	Pro	Cys	Cys	Arg	Pro	Thr	Arg	Tyr	Glu	Ala	Val	
				70					75					80		
tcc	ttc	atg	gac	gtc	aac	agc	acc	tgg	aga	acc	gtg	gac	cgc	ctc	tcc	695
Ser	Phe	Met	Asp	Val	Asn	Ser	Thr	Trp	Arg	Thr	Val	Asp	Arg	Leu	Ser	
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gcc acc gcc tgc ggc tgc ctg ggc tgagggctcg ctccagggct ttgcagactg 749
 Ala Thr Ala Cys Gly Cys Leu Gly
 100 105

gacccttacc ggtggctctt cctgcctggg accctccgc agagtccac tagccagcgg 809

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 -75 -70 -65

Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly
 -60 -55 -50

Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg
 -45 -40 -35

Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
 -30 -25 -20

Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
 -15 -10 -5 -1 1

Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val
 5 10 15

Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg
 20 25 30

Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser
 35 40 45

Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser
 50 55 60 65

Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val
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Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser
85 90 95

Ala Thr Ala Cys Gly Cys Leu Gly
100 105

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<223> DISULFID: Cys43-Cys108 disulfide bridge

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<222> (517)..(711)

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Met Pro Gly Leu Ile Ser Ala Arg Gly Gln Pro Leu Leu Glu

-95

-90

-85

gtc ctt cct ccc caa gcc cac ctg ggt gcc ctc ttt ctc cct gag gct 96

Val Leu Pro Pro Gln Ala His Leu Gly Ala Leu Phe Leu Pro Glu Ala

-80

-75

-70

cca ctt ggt ctc tcc gcg cag cct gcc ctg tgg ccc acc ctg gcc gct 144

Pro Leu Gly Leu Ser Ala Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala

-65

-60

-55

ctg gct ctg ctg agc agc gtc gca gag gcc tcc ctg ggc tcc gcg ccc 192

Leu Ala Leu Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro

-50

-45

-40

cgc agc cct gcc ccc cgc gaa ggc ccc ccg cct gtc ctg gcg tcc ccc 240

Arg Ser Pro Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro

-35

-30

-25

-20

gcc ggc cac ctg ccg ggg gga cgc acg gcc cgc tgg tgc agt gga aga 288

Ala Gly His Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg

-15

-10

-5

gcc cgg cgg ccg ccg ccg cag cct tct cgg ccc gcg ccc ccg ccg cct 336

Ala Arg Arg Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro

-1 1

5

10

gca ccc cca tct gct ctt ccc cgc ggg ggc cgc gcg gcg cgg gct ggg 384
 Ala Pro Pro Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly
 15 20 25

ggc ccg ggc aac cgc gct cgg gca gcg ggg gcg cgg ggc tgc cgc ctg 432
 Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu
 30 35 40 45

cgc tcg cag ctg gtg ccg gtg cgc gcg ctc ggc ctg ggc cac cgc tcc 480
 Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser
 50 55 60

gac gag ctg gtg cgt ttc cgc ttc tgc agc ggc tcc tgc cgc cgc gcg 528
 Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala
 65 70 75

cgc tct cca cac gac ctc agc ctg gcc agc cta ctg ggc gcc ggg gcc 576
 Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala
 80 85 90

ctg cga ccg ccc ccg ggc tcc cgg ccc gtc agc cag ccc tgc tgc cga 624
 Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg
 95 100 105

ccc acg cgc tac gaa gcg gtc tcc ttc atg gac gtc aac agc acc tgg 672
 Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp
 110 115 120 125

aga acc gtg gac cgc ctc tcc gcc aac ccc tgc ggc tgc ctg ggc 717
 Arg Thr Val Asp Arg Leu Ser Ala Asn Pro Cys Gly Cys Leu Gly
 130 135 140

tgagggctcg ctccagggt ttgcagactg gacccttacc ggtggctctt cctgcctggg 777

accctcccgc agagtccac tagccagcgg cctcagccag ggacgaaggc ctcaaagctg 837

agaggcccct gccggtgggt gatg 861

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 -65 -60 -55 -50

Leu Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser
 -45 -40 -35

Pro Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly
 -30 -25 -20

His Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg
 -15 -10 -5

Arg Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro
 -1 1 5 10 15

Pro Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro
 20 25 30

Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser
 35 40 45

Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu
 50 55 60

Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser
 65 70 75

Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg
 80 85 90 95

Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr
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 130 135 140

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<223> Wherein Xaa at position 134 designates Asn or Thr

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<223> Wherein Xaa at position 135 designates Ala or Pro

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20 25 30

Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln
35 40 45

Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
50 55 60

Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
65 70 75 80

His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
85 90 95

Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
100 105 110

Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
115 120 125

Asp Arg Leu Ser Ala Xaa Xaa Cys Gly Cys Leu Gly
130 135 140

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<223> Wherein Xaa at position 110 designates Asn or Thr

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<222> (111)

<223> Wherein Xaa at position 111 designates Ala or Pro

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Arg	Gly	Cys	Arg	Leu	Arg	Ser	Gln	Leu	Val	Pro	Val	Arg	Ala	Leu	Gly
			20					25						30	

Leu	Gly	His	Arg	Ser	Asp	Glu	Leu	Val	Arg	Phe	Arg	Phe	Cys	Ser	Gly
		35						40					45		

Ser	Cys	Arg	Arg	Ala	Arg	Ser	Pro	His	Asp	Leu	Ser	Leu	Ala	Ser	Leu
		50					55					60			

Leu	Gly	Ala	Gly	Ala	Leu	Arg	Pro	Pro	Pro	Gly	Ser	Arg	Pro	Val	Ser
65						70					75				80

Gln	Pro	Cys	Cys	Arg	Pro	Thr	Arg	Tyr	Glu	Ala	Val	Ser	Phe	Met	Asp
				85						90					95

Val	Asn	Ser	Thr	Trp	Arg	Thr	Val	Asp	Arg	Leu	Ser	Ala	Xaa	Xaa	Cys
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Gly	Cys	Leu	Gly
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<223> Wherein Xaa at position 108 designates Ala or Pro

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20 25 30

Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg
35 40 45

Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala
50 55 60

Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys
65 70 75 80

Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser
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Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Xaa Xaa Cys Gly Cys Leu
100 105 110

Gly

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atg gaa ctt gga ctt gga ggc ctc tcc acg ctg tcc cac tgc ccc tgg 105
Met Glu Leu Gly Leu Gly Gly Leu Ser Thr Leu Ser His Cys Pro Trp
-80 -75 -70 -65

cct agg cgg cag cct gcc ctg tgg ccc acc ctg gcc gct ctg gct ctg 153
Pro Arg Arg Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu
-60 -55 -50

ctg agc agc gtc gca gag gcc tcc ctg ggc tcc gcg ccc cgc agc cct	201
Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro	
-45 -40 -35	
gcc ccc cgc gaa ggc ccc ccg cct gtc ctg gcg tcc ccc gcc ggc cac	249
Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His	
-30 -25 -20	
ctg ccg ggg gga cgc acg gcc cgc tgg tgc agt gga aga gcc cgg cgg	297
Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg	
-15 -10 -5 -1	
ccg ccg ccg cag cct tct cgg ccc gcg ccc ccg ccg cct gca ccc cca	345
Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro	
1 5 10 15	
tct gct ctt ccc cgc ggg ggc cgc gcg gcg ccg gct ggg ggc ccg ggc	393
Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly	
20 25 30	
agc cgc gct ccg gca gcg ggg gcg ccg ggc tgc cgc ctg cgc tcg cag	441
Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln	
35 40 45	
ctg gtg ccg gtg cgc gcg ctc ggc ctg ggc cac cgc tcc gac gag ctg	489
Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu	
50 55 60	
gtg cgt ttc cgc ttc tgc agc ggc tcc tgc cgc cgc gcg cgc tct cca	537
Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro	
65 70 75 80	
cac gac ctc agc ctg gcc agc cta ctg ggc gcc ggg gcc ctg cga ccg	585
His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro	
85 90 95	
ccc ccg ggc tcc ccg ccc gtc agc cag ccc tgc tgc cga ccc acg cgc	633
Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg	
100 105 110	
tac gaa gcg gtc tcc ttc atg gac gtc aac agc acc tgg aga acc gtg	681
Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val	
115 120 125	
gac cgc ctc tcc gcc acc gcc tgc ggc tgc ctg ggc tgagggctcg	727
Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly	
130 135 140	

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Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro
-45 -40 -35
Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His
-30 -25 -20
Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg
-15 -10 -5 -1
Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro
1 5 10 15
Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly
20 25 30
Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln
35 40 45
Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
50 55 60
Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
65 70 75 80
His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
85 90 95
Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
100 105 110

Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
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Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
130 135 140

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<223> glycosylated asparagine

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Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln
35 40 45

Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
50 55 60

Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
65 70 75 80

His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
85 90 95

Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
100 105 110

Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
115 120 125

Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
130 135 140

1 5 10 15
 Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His
 20 25 30
 Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg
 35 40 45
 Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala
 50 55 60
 Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys
 65 70 75 80
 Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser
 85 90 95
 Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu
 100 105 110

Gly

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 ccagccctgc tgccgacca cgcgctacga agcggctctc tt 102

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 ttcattggacg tgaacagcac ctggagaacc gtggaccgcc 220

<210> 15
 <211> 2136

<212> DNA

<213> Murinae gen. sp.

<220>

<221> CDS

<222> (975)..(1646)

<400> 15

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cggatccgga ggggtggagcg gccaggtag ccctgaaagg tggggcgggg cgggggcgct 180
ctgggccccca ccccgggatc tggtagcgcc ggggctggaa tttgacaccg gacggcgggc 240
ggcaggaggc tgctgagga tggagttggg ctggccccc agatgcggcc cgcgggctct 300
gccagcaaca agtcctctcg gcccagccc tcgctgcgac tggggcttgg agccctgcac 360
ccaagggcac agaccggctg ccaaggcccc acttttaact aaaagaggcg ctgccagggt 420
cacaactctg ggcctgatcc acttgagctt cgggggaaag cccagcactg gtcccaggag 480
aggcgcttag aaggacacgg accaggacc ctttggtatg gagtgaacgc tgagcatgga 540
gtggaaggaa ctcaagttac tactttctcc aaccaccctg gtaccttcag ccctgaagta 600
cagagcagaa gggctctaga agacaggacc acagctgtgt gagtctcccc cctgaggcct 660
tagacgatct ctgagctcag ctgagctttg tttgcccac tggagaagtg agccattgat 720
tgaccttgtg gcatcgcaa ggaacaggtc ctgccaagca cctaacacag agagcaagg 780
tctccatcgc agctaccgct gctgagttga ctctagctac tccaacctcc tgggtcgctt 840
cgagagactg gagtgggaagg aggaataccc caaaggataa ctaactcatc tttcagtttg 900
caagctgccg caggaagagg gtggggaaac ggtccacga aggcttctga tgggagcttc 960

tggagccgaa agct atg gaa ctg gga ctt gca gag cct act gca ttg tcc 1010
      Met Glu Leu Gly Leu Ala Glu Pro Thr Ala Leu Ser
              1              5              10

cac tgc ctc cgg cct agg tgg cag tca gcc tgg tgg cca acc cta gct 1058
His Cys Leu Arg Pro Arg Trp Gln Ser Ala Trp Trp Pro Thr Leu Ala
      15              20              25
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gtt cta gcc ctg ctg agc tgc gtc aca gaa gct tcc ctg gac cca atg	1106
Val Leu Ala Leu Leu Ser Cys Val Thr Glu Ala Ser Leu Asp Pro Met	
30 35 40	
tcc cgc agc ccc gcc gct cgc gac ggt ccc tca ccg gtc ttg gcg ccc	1154
Ser Arg Ser Pro Ala Ala Arg Asp Gly Pro Ser Pro Val Leu Ala Pro	
45 50 55 60	
ccc acg gac cac ctg cct ggg gga cac act gcg cat ttg tgc agc gaa	1202
Pro Thr Asp His Leu Pro Gly Gly His Thr Ala His Leu Cys Ser Glu	
65 70 75	
aga acc ctg cga ccc ccg cct cag tct cct cag ccc gca ccc ccg ccg	1250
Arg Thr Leu Arg Pro Pro Pro Gln Ser Pro Gln Pro Ala Pro Pro Pro	
80 85 90	
cct ggt ccc gcg ctc cag tct cct ccc gct gcg ctc cgc ggg gca cgc	1298
Pro Gly Pro Ala Leu Gln Ser Pro Pro Ala Ala Leu Arg Gly Ala Arg	
95 100 105	
gcg gcg cgt gca gga acc cgg agc agc cgc gca ccg acc aca gat gcg	1346
Ala Ala Arg Ala Gly Thr Arg Ser Ser Arg Ala Arg Thr Thr Asp Ala	
110 115 120	
cgc ggc tgc cgc ctg cgc tcg cag ctg gtg ccg gtg agc gcg ctc ggc	1394
Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu Gly	
125 130 135 140	
cta ggc cac agc tcc gac gag ctg ata cgt ttc cgc ttc tgc agc ggc	1442
Leu Gly His Ser Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser Gly	
145 150 155	
tcg tgc cgc cga gca cgc tcc cag cac gat ctc agt ctg gcc agc cta	1490
Ser Cys Arg Arg Ala Arg Ser Gln His Asp Leu Ser Leu Ala Ser Leu	
160 165 170	
ctg ggc gct ggg gcc cta cgg tcg cct ccc ggg tcc ccg ccg atc agc	1538
Leu Gly Ala Gly Ala Leu Arg Ser Pro Pro Gly Ser Arg Pro Ile Ser	
175 180 185	
cag ccc tgc tgc cgg ccc act cgc tat gag gcc gtc tcc ttc atg gac	1586
Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp	
190 195 200	
gtg aac agc acc tgg agg acc gtg gac cac ctc tcc gcc act gcc tgc	1634
Val Asn Ser Thr Trp Arg Thr Val Asp His Leu Ser Ala Thr Ala Cys	
205 210 215 220	

ggc tgt ctg ggc tgaggatgat ctatctccaa gcctttgcac actagaccca 1686
Gly Cys Leu Gly

tgtgttgccc tacctggaac agctccaccg ggcctcacta accaggagcc tcaactcagc 1746

aggatatgga ggctgcagag ctcaggcccc aggccggtga gtgacagacg tcgtcggcat 1806

gacagacaga gtgaaagatg tcggaaccac tgaccaacag tcccaagttg ttcattggatc 1866

ccagctctac agacaggaga aacctcagct aaagagaact cctctggggag aatccagaaa 1926

tggccctctg tcctggggaa tgaattttga agagatatat atacatatat acattgtagt 1986

cgcgttgctg gaccagcctg tgctgaaacc agtcccgtgt tcacttgtgg aagccgaagc 2046

cctattttatt atttctaaat tattttattta ctttgaaaaa aaacggccaa gtcggcctcc 2106

cttttagtgag ggtaatttg tgatcccggtg 2136

<210> 16

<211> 224

<212> PRT

<213> Murinae gen. sp.

<400> 16

Met	Glu	Leu	Gly	Leu	Ala	Glu	Pro	Thr	Ala	Leu	Ser	His	Cys	Leu	Arg
1				5					10					15	

Pro	Arg	Trp	Gln	Ser	Ala	Trp	Trp	Pro	Thr	Leu	Ala	Val	Leu	Ala	Leu
			20					25					30		

Leu	Ser	Cys	Val	Thr	Glu	Ala	Ser	Leu	Asp	Pro	Met	Ser	Arg	Ser	Pro
		35						40				45			

Ala	Ala	Arg	Asp	Gly	Pro	Ser	Pro	Val	Leu	Ala	Pro	Pro	Thr	Asp	His
	50					55					60				

Leu	Pro	Gly	Gly	His	Thr	Ala	His	Leu	Cys	Ser	Glu	Arg	Thr	Leu	Arg
65					70					75				80	

Pro	Pro	Pro	Gln	Ser	Pro	Gln	Pro	Ala	Pro	Pro	Pro	Pro	Gly	Pro	Ala
			85					90					95		

Leu	Gln	Ser	Pro	Pro	Ala	Ala	Leu	Arg	Gly	Ala	Arg	Ala	Ala	Arg	Ala
			100					105					110		

Gly Thr Arg Ser Ser Arg Ala Arg Thr Thr Asp Ala Arg Gly Cys Arg

115	120	125
Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu Gly Leu Gly His Ser		
130	135	140
Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg		
145	150	155 160
Ala Arg Ser Gln His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly		
165	170	175
Ala Leu Arg Ser Pro Pro Gly Ser Arg Pro Ile Ser Gln Pro Cys Cys		
180	185	190
Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr		
195	200	205
Trp Arg Thr Val Asp His Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly		
210	215	220

<210> 17
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

<400> 17
 cctggccagc ctactggg 18

<210> 18
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

<400> 18
 aaggagaccg cttagtagcg 20

<210> 19
 <211> 17

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 19
atggaacttg gacttgg

17

<210> 20
<211> 16
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 20
tccatcaccc accggc

16

<210> 21
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 21
ggccaccgct ccgacgag

18

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 22
ggcgggtccac gggttctccag

20

<210> 23
<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 23

ccaagcccac ctgggtgccc tctttctcc

29

<210> 24

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 24

catcacccac cggcaggggc ctctcag

27

<210> 25

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 25

gagcccatgc ccggcctgat ctcagcccga ggaca

35

<210> 26

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 26

ccctggctga ggccgctggc tagtgggact ctgc

34

<210> 27

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization
Probe

<220>

<221> misc_feature

<222> (1)

<223> Wherein n is designated as a, c, t or g

<400> 27

ncaggtggtc cgtggggggc gccaaagaccg g

31

<210> 28

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 28

ctaggagccc atgccc

16

<210> 29

<211> 351

<212> DNA

<213> Homo sapiens

<400> 29

atggctggag gaccgggata tcgtgctcgt gcagcaggag cacgtggctg tcgtctgcgt 60
tctcaactag tgccggtgcg tgactcgga ctgggacacc gttccgacga actagtacgt 120
tttcgttttt gtccaggatc ttgtcgtcgt gcacgtttctc cgcgatgatct atctctagca 180
tctctactag gagccggagc actaagaccg ccgccgggat ctagacctgt atctcaacct 240
tggtgtagac ctactagata cgaagcagta tctttcatgg acgtaaactc tacatggaga 300
accgtagata gactatctgc aaccgcatgt ggctgtctag gatgataata g 351

<210> 30

<211> 414

<212> DNA

<213> Homo sapiens

<400> 30


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atggggccatc atcatcatca tcatcatcat catcactcga gcggccatat cgacgacgac 60
gacaaggctg gaggaccggg atctcgtgct cgtgcagcag gagcacgtgg ctgtcgtctg 120
cgttctcaac tagtgccggt gcgtgcactc ggactgggac accgttccga cgaactagta 180
cgttttcgtt tttgttcagg atcttgctgt cgtgcacgtt ctccgcatga tctatctcta 240
gcatctctac taggagccgg agcactaaga ccgccgccgg gatctagacc tgtatctcaa 300
ccttgttgta gacctactag atacgaagca gtatctttca tggacgtaaa ctctacatgg 360
agaaccgtag atagactatc tgcaaccgca tgtggctgtc taggatgata atag      414

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<210> 31
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 31
 aaggaaaaaa gcggccgcca tggaacttgg acttgagg 39

<210> 32
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 32
 ttttttcctt ggccggccgct cagcccaggc agccgcagg 39

<210> 33
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 33
 gagcgagccc tcagcc 16

<210> 34
 <211> 197
 <212> PRT

<213> Homo sapiens

<400> 34

Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
1 5 10 15

Val Leu Ser Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg
20 25 30

Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp
35 40 45

Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
50 55 60

Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
65 70 75 80

Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Ala
85 90 95

Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val
100 105 110

Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg
115 120 125

Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly
130 135 140

Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val Arg
145 150 155 160

Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe
165 170 175

Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala Arg
180 185 190

Glu Cys Ala Cys Val
195

<210> 35

<211> 220

<212> PRT

<213> Homo sapiens

<210> 11
<211> 116
<212> PRT
<213> Homo sapiens

<220>
<221> CARBOHYD
<222> (98)
<223> glycosylated asparagine

<400> 11
Ala Ala Arg Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala
1 5 10 15
Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly
20 25 30
Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly
35 40 45
Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu
50 55 60
Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser
65 70 75 80
Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp
85 90 95
Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys
100 105 110
Gly Cys Leu Gly
115

<210> 12
<211> 113
<212> PRT
<213> Homo sapiens

<220>
<221> CARBOHYD
<222> (95)
<223> glycosylated asparagine

<400> 12
Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys

<400> 35

Met Glu Leu Gly Leu Gly Gly Leu Ser Thr Leu Ser His Cys Pro Trp
1 5 10 15

Pro Arg Arg Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu
20 25 30

Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro
35 40 45

Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His
50 55 60

Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg
65 70 75 80

Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro
85 90 95

Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly
100 105 110

Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln
115 120 125

Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
130 135 140

Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
145 150 155 160

His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
165 170 175

Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
180 185 190

Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
195 200 205

Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
210 215 220

<210> 36

<211> 156

<212> PRT

<213> Homo sapiens

<400> 36

Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Leu Ser Leu
1 5 10 15

Gln Leu Gly Gln Gly Trp Gly Pro Asp Ala Arg Gly Val Pro Val Ala
20 25 30

Asp Gly Glu Phe Ser Ser Glu Gln Val Ala Lys Ala Gly Gly Thr Trp
35 40 45

Leu Gly Thr His Arg Pro Leu Ala Arg Leu Arg Arg Ala Leu Ser Gly
50 55 60

Pro Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala Glu Leu Gly Leu
65 70 75 80

Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser
85 90 95

Cys Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala Leu Ala Arg Leu
100 105 110

Gln Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys Arg Pro Thr Arg
115 120 125

Tyr Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg Trp Gln Arg Leu
130 135 140

Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
145 150 155

<210> 37

<211> 211

<212> PRT

<213> Homo sapiens

<400> 37

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
1 5 10 15

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala Pro
20 25 30

Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser
35 40 45

Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val
 50 55 60

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp
 65 70 75 80

Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala
 85 90 95

Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
 100 105 110

Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr
 115 120 125

Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr
 130 135 140

Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu
 145 150 155 160

Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln
 165 170 175

Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
 180 185 190

Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys
 195 200 205

Gly Cys Ile
 210

<210> 38
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 38
 gctggccccg ctgcaggg

<210> 39
 <211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 39

gctgcgacga ctgcgcca

18

<210> 40

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 40

attgaaaaac ttatccag

18

<210> 41

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 41

taggccacgt cggtgtagcg

20

<210> 42

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 42

aaggacacct cgtcctcgta ggc

23

<210> 43

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 43

aacgacaggt catcatcaaa ggc